

SEQ SEARCH SUMMARY

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 15, 2003, 15:22:07 ; Search time 14903 Seconds
(without alignments)
5492.865 Million cell updates/sec

Title: US-10-018-929A-3 amino acid
Perfect score: 10277
Sequence: 1 MKKDEKIGLTGRTIYTRSLA.....QSLSSGLQSNNEVCLSDDE 2001

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

in DNA databases

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp

Q=/cgn2_1/USPTO_spool_p/US10018929/runat_14112003_101422_18817/app_query.fasta_1.2183

-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10018929_CGN_1_1_10588_atrunat_14112003_101422_18817 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*

Also searched SEQ ID NO:2
in DNA databases with
same results.

DNA

11: gb_sts:*
 12: gb_sy:*
 13: gb_un:*
 14: gb_vi:*
 15: em_ba:*
 16: em_fun:*
 17: em_hum:*
 18: em_in:*
 19: em_mu:*
 20: em_om:*
 21: em_or:*
 22: em_ov:*
 23: em_pat:*
 24: em_ph:*
 25: em_pl:*
 26: em_ro:*
 27: em_sts:*
 28: em_un:*
 29: em_vi:*
 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htg_mus:*
 34: em_htg_pln:*
 35: em_htg_rod:*
 36: em_htg_mam:*
 37: em_htg_vrt:*
 38: em_sy:*
 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length					
	1	10277	100.0	6554	8	AF213627			AF213627 Arabidops
	2	10277	100.0	6571	6	AX063583			AX063583 Sequence
	3	9500	92.4	10329	6	AX063582			AX063582 Sequence
	4	9491	92.4	10329	8	AF213628			AF213628 Arabidops
c	5	9491	92.4	120965	8	AC026875			AC026875 Genomic s
	6	1237	12.0	939	8	AK117959			AK117959 Arabidops
	7	1177	11.5	702	8	BT006219			BT006219 Arabidops
	8	1033	10.1	695	8	ATH552638			ATH552638 Arabidops
c	9	689.5	6.7	519	6	AX063607			AX063607 Sequence
c	10	638.5	6.2	184118	8	AP005621			AP005621 Oryza sat
	11	578	5.6	150597	2	AP005005			AP005005 Oryza sat
c	12	578	5.6	156316	2	AP004752			AP004752 Oryza sat
	13	494.5	4.8	467	6	AX063609			AX063609 Sequence
	14	472	4.6	515	6	AX063611			AX063611 Sequence
	15	393	3.8	2282	8	BT003975			BT003975 Arabidops
	16	392.5	3.8	2014	8	BT004948			BT004948 Arabidops

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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 15, 2003, 08:58:56 ; Search time 1001 Seconds
(without alignments)
5396.179 Million cell updates/sec

Title: US-10-018-929A-3
Perfect score: 10277
Sequence: 1 MKKDEKIGLTGRTIYTRSLA.....QSLSSGLQSNNEVCLSDDE 2001

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp

Q=/cgn2_1/USPTO_spool_p/US10018929/runat_14112003_101422_18807/app_query.fasta_1
.2183

-DB=N_Geneseq_19Jun03 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10018929_CGN_1_1_819@runat_14112003_101422_18807 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_19Jun03:*
1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*

11: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
 12: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
 13: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
 14: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
 15: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
 16: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
 17: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
 18: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
 19: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
 20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
 21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
 22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
 23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
 24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
 25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length	Match	Length			
	1	10277	100.0	6571	22	AAA89354			Arabidopsis thalia
	2	9500	92.4	10329	22	AAA89353			Arabidopsis thalia
	3	9491	92.4	10329	22	AAA89385			Arabidopsis thalia
c	4	689.5	6.7	519	22	AAA89377			Brassica oleracea
	5	494.5	4.8	467	22	AAA89379			Brassica oleracea
	6	472	4.6	515	22	AAA89381			Brassica oleracea
	7	378	3.7	419	22	AAA89378			Brassica oleracea
	8	366.5	3.6	11597	23	ABL23160			Drosophila melanog
	9	359	3.5	8307	23	ABL23161			Drosophila melanog
	10	355	3.5	9953	23	ABL21371			Drosophila melanog
	11	330	3.2	6025	23	ABL29649			Drosophila melanog
	12	329.5	3.2	10136	17	AAT34578			Kinetochore protei
	13	327.5	3.2	9035	24	ABK89430			Human tumour suppr
	14	327.5	3.2	9229	25	ABX34821			Human mddt cDNA SE
	15	327	3.2	18506	23	ABL05592			Drosophila melanog
	16	325.5	3.2	10342	25	ABZ36315			Human secretory po
c	17	325	3.2	574	22	AAA89382			Brassica oleracea
c	18	324.5	3.2	7303	23	ABL29648			Drosophila melanog
	19	324.5	3.2	10096	24	ABK70292			Human lung cancer
	20	324.5	3.2	10096	25	ABX10341			DNA encoding prote
	21	319.5	3.1	31497	25	ABX72626			Human cDNA encodin
	22	318	3.1	7409	23	ABL13405			Drosophila melanog
c	23	318	3.1	10215	23	ABL13404			Drosophila melanog
	24	317.5	3.1	6364	25	ACA04019			cDNA downregulated
	25	317.5	3.1	8789	16	AAQ86851			Human mitosin gene
	26	317.5	3.1	8789	19	AAV09076			Mitosin nucleic ac
	27	317.5	3.1	10190	24	ABK09755			Human ovarian tumo
	28	317.5	3.1	10211	24	ABT11010			Human breast cance
	29	317.5	3.1	10211	24	ABL65843			Lung cancer relate
	30	317.5	3.1	10211	24	ABL67994			Ovary cancer relat
	31	316.5	3.1	12629	23	ABL21370			Drosophila melanog
	32	311.5	3.0	10281	24	AAS94946			Human DNA sequence

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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 15, 2003, 18:41:28 ; Search time 260 Seconds
(without alignments)
3396.952 Million cell updates/sec

Title: US-10-018-929A-3
Perfect score: 10277
Sequence: 1 MKKDEKIGLTGRTIYTRSLA.....QSLSSGLQSNNEVCLSDDE 2001

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp

Q=/cgn2_1/USPTO_spool_p/US10018929/runat_14112003_101423_18850/app_query.fasta_1
.2183

-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10018929_@CGN_1_1_160_@runat_14112003_101423_18850 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	329.5	3.2	10136	1	US-08-353-700-2	Sequence 2, Appli
2	329.5	3.2	10136	5	PCT-US95-16216-2	Sequence 2, Appli
3	317.5	3.1	8789	1	US-08-328-254-5	Sequence 5, Appli
4	305	3.0	6328	4	US-08-913-832A-1	Sequence 1, Appli
5	305	3.0	6328	4	US-09-249-181A-1	Sequence 1, Appli
6	305	3.0	6328	4	US-09-158-707-1	Sequence 1, Appli
7	305	3.0	6475	4	US-09-620-312D-325	Sequence 325, App
8	288	2.8	30549	4	US-09-134-001C-322	Sequence 322, App
9	278.5	2.7	6773	4	US-09-166-350-27	Sequence 27, Appl
10	275	2.7	11091	4	US-09-134-001C-2243	Sequence 2243, Ap
11	268.5	2.6	2512	4	US-09-702-705-1802	Sequence 1802, Ap
12	268.5	2.6	2512	4	US-09-736-457-1802	Sequence 1802, Ap
13	266.5	2.6	5200	4	US-08-978-277A-3	Sequence 3, Appli
14	266	2.6	5471	4	US-09-535-008-1	Sequence 1, Appli
15	266	2.6	5471	4	US-09-535-008-62	Sequence 62, Appl
16	264.5	2.6	5468	4	US-09-535-008-66	Sequence 66, Appl
17	264.5	2.6	5480	4	US-09-535-008-70	Sequence 70, Appl
18	263	2.6	5477	4	US-09-535-008-74	Sequence 74, Appl
19	263	2.6	5567	4	US-09-535-008-64	Sequence 64, Appl
20	262.5	2.6	5576	4	US-09-535-008-72	Sequence 72, Appl
21	262	2.5	5386	4	US-09-535-008-60	Sequence 60, Appl
22	257.5	2.5	14770	4	US-09-220-132-30	Sequence 30, Appl
23	255.5	2.5	5564	4	US-09-535-008-68	Sequence 68, Appl
24	254	2.5	5573	4	US-09-535-008-76	Sequence 76, Appl
25	251	2.4	6608	4	US-09-220-132-58	Sequence 58, Appl
26	250.5	2.4	5857	4	US-09-220-132-79	Sequence 79, Appl
27	249	2.4	8257	4	US-09-595-684B-30	Sequence 30, Appl
28	248	2.4	8503	4	US-09-620-312D-130	Sequence 130, App
29	244.5	2.4	6605	1	US-08-769-309A-4	Sequence 4, Appli
30	244.5	2.4	6605	3	US-08-994-570-4	Sequence 4, Appli
31	243.5	2.4	5736	4	US-09-854-856-63	Sequence 63, Appl
32	243.5	2.4	5916	4	US-09-854-856-31	Sequence 31, Appl
33	243.5	2.4	6147	4	US-09-854-856-61	Sequence 61, Appl
34	243.5	2.4	6327	4	US-09-854-856-29	Sequence 29, Appl
35	237	2.3	6337	4	US-09-620-312D-1063	Sequence 1063, Ap
36	232.5	2.3	6654	4	US-09-854-856-19	Sequence 19, Appl
37	232.5	2.3	7065	4	US-09-854-856-17	Sequence 17, Appl
38	231.5	2.3	5820	4	US-09-854-856-47	Sequence 47, Appl
39	231.5	2.3	6000	4	US-09-854-856-15	Sequence 15, Appl
40	231.5	2.3	6231	4	US-09-854-856-45	Sequence 45, Appl
41	231.5	2.3	6411	4	US-09-854-856-13	Sequence 13, Appl
42	231	2.2	6195	4	US-09-854-856-25	Sequence 25, Appl
43	231	2.2	6606	4	US-09-854-856-23	Sequence 23, Appl
44	229.5	2.2	3436	3	US-09-276-531-60	Sequence 60, Appl
45	229	2.2	11283	2	US-08-603-753D-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-08-353-700-2

; Sequence 2, Application US/08353700

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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 15, 2003, 19:13:58 ; Search time 1276 Seconds
(without alignments)
5125.139 Million cell updates/sec

Title: US-10-018-929A-3
Perfect score: 10277
Sequence: 1 MKKDEKIGLTGRTIYTRSLA.....QSLSSGLQSNNEVCLSDDE 2001

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2169961 seqs, 1634102185 residues

Total number of hits satisfying chosen parameters: 4339922

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp

-Q=/cgn2_1/USPTO_spool_p/US10018929/runat_14112003_101424_18873/app_query.fasta_1
.2183

-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10018929 @CGN_1_1_185 @runat_14112003_101424_18873
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
 15: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
 16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
 17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	327.5	3.2	7764	12	US-09-814-353-21548	Sequence 21548, A
2	324.5	3.2	10096	10	US-09-960-253-163	Sequence 163, App
3	317.5	3.1	6364	13	US-10-071-766-140	Sequence 140, App
4	317.5	3.1	10190	10	US-09-864-864-292	Sequence 292, App
5	317.5	3.1	10211	10	US-09-954-456-1153	Sequence 1153, Ap
6	317.5	3.1	10211	10	US-09-967-768A-186	Sequence 186, App
7	317.5	3.1	10211	11	US-09-918-624B-2	Sequence 2, Appli
8	314	3.1	10281	14	US-10-084-817-361	Sequence 361, App
9	311.5	3.0	10281	12	US-10-240-965-201	Sequence 201, App
10	305	3.0	5739	10	US-09-960-253-142	Sequence 142, App
11	305	3.0	5901	12	US-09-849-602-1	Sequence 1, Appli
12	305	3.0	6417	9	US-09-962-436-288	Sequence 288, App
13	305	3.0	6417	12	US-10-096-534-28	Sequence 28, Appl
14	305	3.0	6475	14	US-10-037-270-325	Sequence 325, App
15	298	2.9	7694	12	US-10-096-534-34	Sequence 34, Appl
16	298	2.9	8063	12	US-09-814-353-21776	Sequence 21776, A
17	288	2.8	8730	13	US-10-124-800-1	Sequence 1, Appli
18	284.5	2.8	7497	10	US-09-960-253-175	Sequence 175, App
19	284.5	2.8	7792	13	US-10-044-090-359	Sequence 359, App
20	279	2.7	6608	7	US-08-973-363-10	Sequence 10, Appl
21	278.5	2.7	6773	10	US-09-864-864-336	Sequence 336, App
22	278.5	2.7	8413	9	US-09-801-574-7	Sequence 7, Appli
23	277.5	2.7	8370	9	US-09-801-574-56	Sequence 56, Appl
24	274.5	2.7	7805	12	US-10-006-285-400	Sequence 400, App
25	274.5	2.7	7805	13	US-10-044-090-370	Sequence 370, App
26	274	2.7	6354	14	US-10-084-817-158	Sequence 158, App
27	272	2.6	3901	10	US-09-834-975-1043	Sequence 1043, Ap
28	272	2.6	7035	9	US-09-815-242-8615	Sequence 8615, Ap
29	269	2.6	6331	14	US-10-175-523-51	Sequence 51, Appl
30	269	2.6	9027	12	US-09-930-213-304	Sequence 304, App
31	268.5	2.6	2512	10	US-09-736-457-1802	Sequence 1802, Ap
32	268.5	2.6	2512	10	US-09-902-941-1802	Sequence 1802, Ap
33	268.5	2.6	2512	10	US-09-849-626-1802	Sequence 1802, Ap
34	268.5	2.6	2512	12	US-10-113-872-1802	Sequence 1802, Ap
35	268.5	2.6	2512	14	US-10-017-754-1802	Sequence 1802, Ap
36	266.5	2.6	6160	10	US-09-902-432-3	Sequence 3, Appli
37	266	2.6	3219	10	US-09-925-300-737	Sequence 737, App
38	265	2.6	7434	9	US-09-815-242-4761	Sequence 4761, Ap
39	265	2.6	7437	9	US-09-815-242-8869	Sequence 8869, Ap
40	265	2.6	12258	9	US-09-801-574-58	Sequence 58, Appl
41	264.5	2.6	31096	8	US-08-781-986A-59	Sequence 59, Appl

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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 15, 2003, 18:34:43 ; Search time 7607 Seconds
(without alignments)
6393.224 Million cell updates/sec

Title: US-10-018-929A-3
Perfect score: 10277
Sequence: 1 MKKDEKIGLTGRTIYTRSLA.....QSLSSGLQSNNEVVCLSDDE 2001

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp

Q=/cgn2_1/USPTO_spool_p/US10018929/runat_14112003_101423_18829/app_query.fasta_1
.2183

-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10018929 @CGN_1_1_5892 @runat_14112003_101423_18829 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*

12: gb_est3:*
 13: gb_est4:*
 14: gb_est5:*
 15: em_estfun:*
 16: em_estom:*
 17: em_gss_hum:*
 18: em_gss_inv:*
 19: em_gss_pln:*
 20: em_gss_vrt:*
 21: em_gss_fun:*
 22: em_gss_mam:*
 23: em_gss_mus:*
 24: em_gss_pro:*
 25: em_gss_rod:*
 26: em_gss_phg:*
 27: em_gss_vrl:*
 28: gb_gssl:*
 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					Description
Result	Query	Match	Length	DB	ID		
No.	Score						
c	1	1178	11.5	719	28	AQ956407	AQ956407 LERAJ80TF
	2	1075	10.5	769	28	AQ956408	AQ956408 LERAJ80TR
	3	961	9.4	635	9	AU238798	AU238798 AU238798
	4	730	7.1	432	10	BE525189	BE525189 M59F2STM
	5	711	6.9	416	29	CNS00UQL	AL091323 Arabidops
c	6	654	6.4	1034	29	BZ505855	BZ505855 BONHA49TF
	7	603.5	5.9	811	28	B20116	B20116 T7K21-T7 TA
c	8	569	5.5	767	28	BH706682	BH706682 BOMPS61TR
	9	508.5	4.9	791	29	BZ505861	BZ505861 BONHA49TR
	10	506.5	4.9	942	28	B08967	B08967 F4J17-T7 IG
	11	491	4.8	310	29	BZ358017	BZ358017 SALK_1317
	12	489.5	4.8	928	28	B11993	B11993 F3G11-T7 IG
	13	473	4.6	448	29	CNS00NS6	AL082308 Arabidops
c	14	448.5	4.4	712	28	BH980252	BH980252 ode69f11.
	15	437.5	4.3	690	28	BH978547	BH978547 odf89d10.
	16	430	4.2	258	10	BE526124	BE526124 M64B06STM
c	17	426	4.1	728	28	BH419722	BH419722 BOGOE69TR
	18	424.5	4.1	729	28	BZ072045	BZ072045 lkg27d05.
	19	413	4.0	654	28	BH989471	BH989471 oem85a08.
c	20	389.5	3.8	526	29	BZ492259	BZ492259 BONAJS3TF
	21	380.5	3.7	764	28	B21274	B21274 F4J17-T7.1
	22	379	3.7	407	29	CNS00N9H	AL081635 Arabidops
c	23	378.5	3.7	766	28	BH979060	BH979060 ode71c04.
c	24	322	3.1	398	9	AU230038	AU230038 AU230038
c	25	310.5	3.0	684	29	BZ465288	BZ465288 BONRU74TR
c	26	310	3.0	560	28	BH788688	BH788688 fzm021f0
	27	299.5	2.9	369	28	BH419713	BH419713 BOGOE69TF
c	28	289	2.8	512	28	BH707844	BH707844 BOMHE27TF
	29	284.5	2.8	482	12	BG833434	BG833434 951008C07